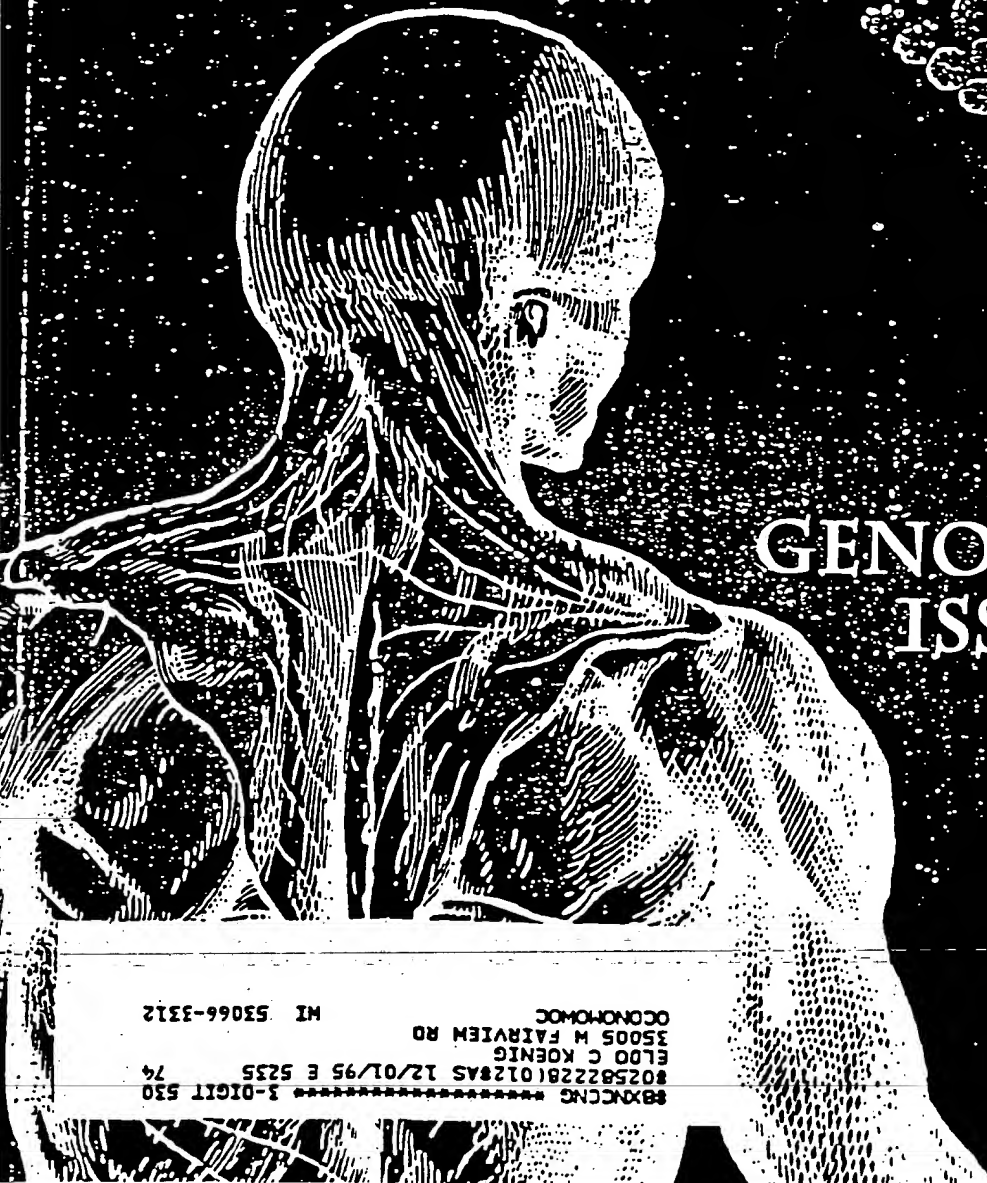


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# SCIENTIFIC AMERICAN

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## GENOME ISSUE

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Genome Project adds a new dimension to questions of gene expression in humans and model systems. A report on page 415 summarizes progress in the *enorhabditis elegans* Genome Project and indicates new ways information about sequences can be used.

News stories, Articles, Perspectives, Policy Forums, and Reports focus on technological developments, clinical applications, and ethical concerns resulting from the burgeoning of genomic information. [*C. elegans* image: F. Maduro and D. Pilgrim, University of Alberta]



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Axl1p sequence following Ser<sup>205</sup> and occurs within the C-terminus of Axl1p that shows homology with hDE (14). To delete the complete STE23 sequence and create the ste23Δ:URA3 mutation, polymerase chain reaction (PCR) primers (5'-TCGGAAGACCTCAT-TCTTGTCTATTTTGATTTGCTC- TGATAGTTG-TACTGAGAGTGCAC-3'; and 5'-GCTACAAACAGC-GTCGACTTGAATGCCCGACATCTTCGACTGT-GCGGTATTTTACACCG-3') were used to amplify the URA3 sequence of pRS316, and the reaction product was transformed into yeast for one-step gene replacement [R. Rothstein, *Methods Enzymol.* 194, 281 (1991)]. To create the axl1Δ::LEU2 mutation contained on p114, a 5.0-kb Sal I fragment from pAXL1 was cloned into pUC19, and an internal 4.0-kb Hpa I-Xho I fragment was replaced with a LEU2 fragment. To construct the ste23Δ::LEU2 allele (a deletion corresponding to 831 amino acids) carried on p153, a LEU2 fragment was used to replace the 2.8-kb Pml I-Ecl136 II fragment of STE23, which occurs within a 6.2-kb Hind III-Bgl II genomic fragment carried on pSP72 (Promega). To create YEP<sup>MAF1</sup>, a 1.6-kb Bam HI fragment containing MFA1, from pKK16 [K. Kuchler, R. E. Sterne, J. Thorer, *EMBO J.* 8, 3973 (1989)], was ligated into the Bam HI site of YEP351 [J. E. Hill, A. M. Myers, T. J. Koerner, A. Tzagoloff, *Yeast* 2, 163 (1986)]. J. Chant and I. Herskowitz, *Cell* 65, 1203 (1991). B. W. Matthews, *Acc. Chem. Res.* 21, 333 (1988). K. Kuchler, H. G. Dohman, J. Thorer, *J. Cell Biol.* 120, 1203 (1993); R. Koling and C. P. Hollenberg, *EMBO J.* 13, 3261 (1994); C. Benkower, D. Loayza, S. Michaels, *Mol. Biol. Cell* 5, 1185 (1994). A. Bender and J. R. Pringle, *Proc. Natl. Acad. Sci. USA* 86, 9976 (1989); J. Chant, K. Corrado, J. R. Pringle, I. Herskowitz, *Cell* 65, 1213 (1991); S. Powers, E. Gonzales, T. Christensen, J. Cubert, D. Broek, *ibid.*, p. 1225; H. O. Park, J. Chant, I. Herskowitz, *Nature* 365, 269 (1993); J. Chant, *Trends Genet.* 10, 328 (1994); — and J. R. Pringle, *J. Cell Biol.* 129, 751 (1995); J. Chant, M. Mischke, E. Mitchell, I. Herskowitz, J. R. Pringle, *ibid.*, p. 767. G. F. Sprague Jr., *Methods. Enzymol.* 194, 77 (1991).

Single-letter abbreviations for the amino acid residues are as follows: A, Ala; C, Cys; D, Asp; E, Glu; F, Phe; G, Gly; H, His; I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gln; R, Arg; S, Ser; T, Thr; V, Val; W, Trp; and Y, Tyr.

A W303 1A derivative, SY2625 (MATa ura3-1 leu2-3, 112 trp1-1 ade2-1 can1-100 ss11Δ mfa2Δ::FUS1-lacZ his3Δ::FUS1-HIS3), was the parent strain for the mutant search. SY2625 derivatives for the mating assays, secreted pheromone assays, and the pulse-chase experiments included the following strains: Y49 (ste22-1), Y115 (mfa1Δ::LEU2), Y142 (axl1::URA3), Y173 (axl1Δ::LEU2), Y220 (axl1::URA3 ste23Δ::URA3), Y221 (ste23Δ::URA3), Y231 (axl1Δ::LEU2 ste23Δ::LEU2), and Y233 (ste23Δ::LEU2). MATa derivatives of SY2625 included the following strains: Y199 (SY2625 made MATa), Y278 (ste22-1), Y195 (mfa1Δ::LEU2), Y196 (axl1Δ::LEU2), and Y197 (axl1::URA3). The EG123 (MATa leu2 ura3 trp1 can1 his4) genetic background was used to create a set of strains for analysis of bud site selection. EG123 derivatives included the following strains: Y175 (axl1Δ::LEU2), Y223 (axl1::URA3), Y234 (ste23Δ::LEU2), and Y272 (axl1Δ::LEU2 ste23Δ::LEU2). MATa derivatives of EG123 included the following strains: Y214 (EG123 made MATa) and Y293 (axl1Δ::LEU2). All strains were generated by means of standard genetic or molecular methods involving the appropriate constructs (23). In particular, the axl1 ste23 double mutant strains were created by crossing of the appropriate MATa ste23 and MATa axl1 mutants, followed by sporulation of the resultant diploid and isolation of the double mutant from nonparental di-type tetrads. Gene disruptions were confirmed with either PCR or Southern (DNA) analysis.

p129 is a YEP352 [J. E. Hill, A. M. Myers, T. J. Koerner, A. Tzagoloff, *Yeast* 2, 163 (1986)] plasmid containing a 5.5-kb Sal I fragment of pAXL1. p151 was derived from p129 by insertion of a linker at the Bgl II site within AXL1, which led to an in-frame insertion of the hemagglutinin (HA) epitope (DQYPYDVPDYA) (29) between amino acids 854 and 855 of the AXL1 prod-

uct. pC225 is a KS+ (Stratagene) plasmid containing a 0.5-kb Bam HI-Sal I fragment from pAXL1. Substitution mutations of the proposed active site of Axl1p were created with the use of pC225 and site-specific mutagenesis involving appropriate synthetic oligonucleotides (axl1-H68A, 5'-GTGCTCACAAGCGCT-GCCAAACCGGC-3'; axl1-E71A, 5'-AAGAATCAT-GTGCGCACAAAGGTGCGC-3'; and axl1-E71D, 5'-AAGAATCATGTGATCACAAGGTGCGC-3'). The mutations were confirmed by sequence analysis. After mutagenesis, the 0.4-kb Bam HI-Msc I fragment from the mutagenized pC225 plasmids was transferred into pAXL1 to create a set of pRS316 plasmids carrying different AXL1 alleles, p124 (axl1-H68A), p130 (axl1-E71A), and p132 (axl1-E71D). Similarly, a set of HA-tagged alleles carried on YEP352 were created after replacement of the p151 Bam HI-Msc I fragment, to generate p161 (axl1-E71A), p162 (axl1-

H68A), and p163 (axl1-E71D).

32. We thank J. Becker and S. Michaels for providing a-factor antibodies; S. Michaels for discussing unpublished results and helping with the pulse-chase experiments; J. Brown, J. Chant, and S. Sanders for their input concerning bud site selection experiments; M. Raymond, F. Tamanoi, and M. Whiteway for plasmids; M. Marra for providing the STE23 genomic fragment; and H. Bussey, J. Brown, N. Davis, T. Favero, C. de Hoog, and S. Kim for comments on the manuscript. Supported by a grant to C.B. from the Natural Sciences and Engineering Research Council of Canada. Support for M.N.A. was from a California Tobacco-Related Disease Research Program postdoctoral fellowship (4FT-0083).

22 June 1995; accepted 21 August 1995

## Quantitative Monitoring of Gene Expression Patterns with a Complementary DNA Microarray

Mark Schena,\* Dari Shalon,\*† Ronald W. Davis, Patrick O. Brown‡

A high-capacity system was developed to monitor the expression of many genes in parallel. Microarrays prepared by high-speed robotic printing of complementary DNAs on glass were used for quantitative expression measurements of the corresponding genes. Because of the small format and high density of the arrays, hybridization volumes of 2 microliters could be used that enabled detection of rare transcripts in probe mixtures derived from 2 micrograms of total cellular messenger RNA. Differential expression measurements of 45 *Arabidopsis* genes were made by means of simultaneous, two-color fluorescence hybridization.

The temporal, developmental, topographical, histological, and physiological patterns in which a gene is expressed provide clues to its biological role. The large and expanding database of complementary DNA (cDNA) sequences from many organisms (1) presents the opportunity of defining these patterns at the level of the whole genome.

For these studies, we used the small flowering plant *Arabidopsis thaliana* as a model organism. *Arabidopsis* possesses many advantages for gene expression analysis, including the fact that it has the smallest genome of any higher eukaryote examined to date (2). Forty-five cloned *Arabidopsis* cDNAs (Table 1), including 14 complete sequences and 31 expressed sequence tags (ESTs), were used as gene-specific targets. We obtained the ESTs by selecting cDNA clones at random from an *Arabidopsis* cDNA library. Sequence analysis revealed that 28 of the 31 ESTs matched sequences

in the database (Table 1). Three additional cDNAs from other organisms served as controls in the experiments.

The 48 cDNAs, averaging ~1.0 kb, were amplified with the polymerase chain reaction (PCR) and deposited into individual wells of a 96-well microtiter plate. Each sample was duplicated in two adjacent wells to allow the reproducibility of the arraying and hybridization process to be tested. Samples from the microtiter plate were printed onto glass microscope slides in an area measuring 3.5 mm by 5.5 mm with the use of a high-speed arraying machine (3). The arrays were processed by chemical and heat treatment to attach the DNA sequences to the glass surface and denature them (3). Three arrays, printed in a single lot, were used for the experiments here. A single microtiter plate of PCR products provides sufficient material to print at least 500 arrays.

Fluorescent probes were prepared from total *Arabidopsis* mRNA (4) by a single round of reverse transcription (5). The *Arabidopsis* mRNA was supplemented with human acetylcholine receptor (AChR) mRNA at a dilution of 1:10,000 (w/w) before cDNA synthesis, to provide an internal standard for calibration (5). The resulting fluorescently labeled cDNA mixture was hybridized to an array at high stringency (6) and scanned

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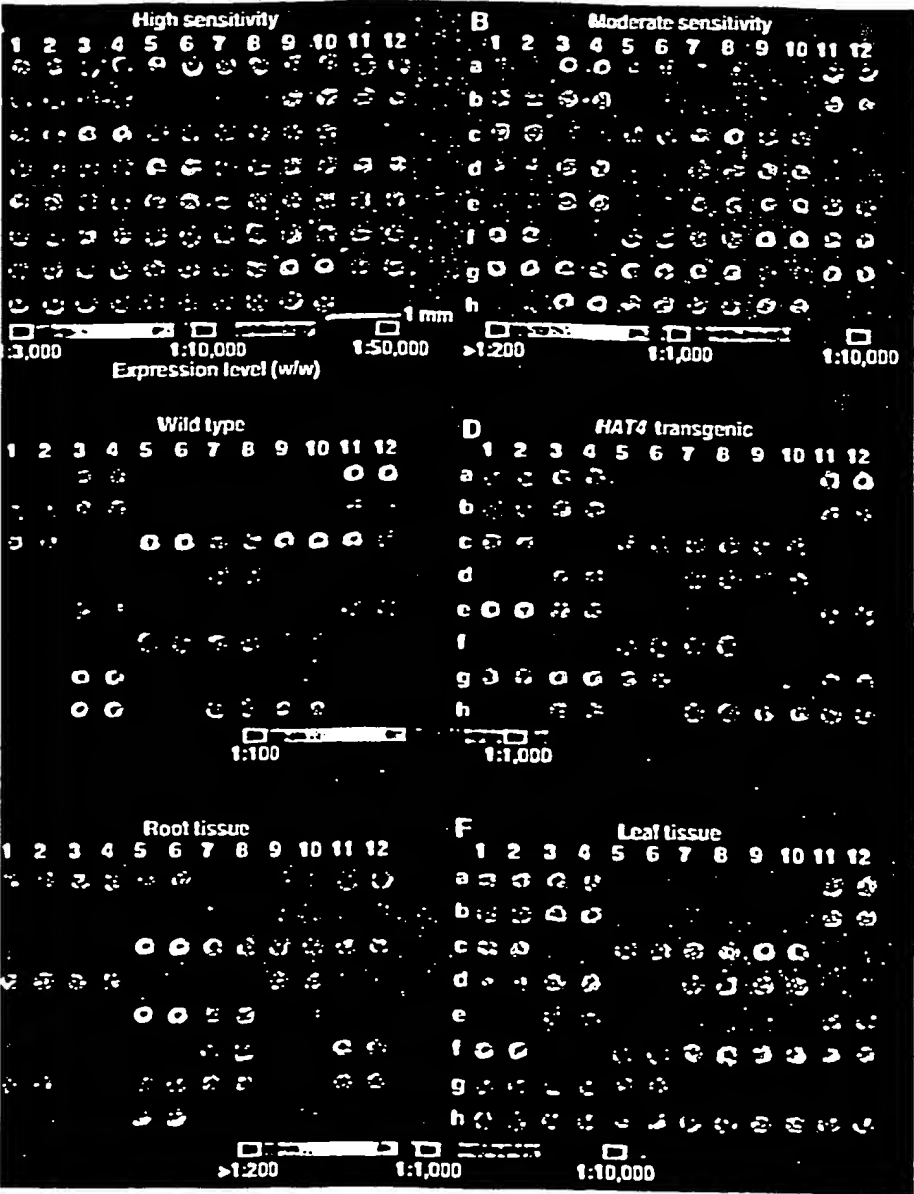
a laser (3). A high-sensitivity scan gave  
als that saturated the detector at nearly  
of the *Arabidopsis* target sites (Fig. 1A).  
ibration relative to the AChR mRNA  
dard (Fig. 1A) established a sensitivity  
t of ~1:50,000. No detectable hybridiza-  
was observed to either the rat glucocor-  
id receptor (Fig. 1A) or the yeast TRP4  
. 1A) targets even at the highest scan-  
g sensitivity. A moderate-sensitivity scan

of the same array allowed linear detection of  
the more abundant transcripts (Fig. 1B).  
Quantitation of both scans revealed a range  
of expression levels spanning three orders of  
magnitude for the 45 genes tested (Table 2).  
RNA blots (7) for several genes (Fig. 2)  
corroborated the expression levels measured  
with the microarray to within a factor of 5  
(Table 2).

Differential gene expression was investi-

gated with a simultaneous, two-color hy-  
bridization scheme, which served to mini-  
mize experimental variation inherent in the  
comparison of independent hybridizations.  
Fluorescent probes were prepared from two  
mRNA sources with the use of reverse tran-  
scriptase in the presence of fluorescein- and  
lissamine-labeled nucleotide analogs, re-  
spectively (5). The two probes were then  
mixed together in equal proportions, hy-  
bridized to a single array, and scanned se-  
parately for fluorescein and lissamine emis-  
sion after independent excitation of the two  
fluorophores (3).

To test whether overexpression of a sin-  
gle gene could be detected in a pool of total  
*Arabidopsis* mRNA, we used a microarray t  
analyze a transgenic line overexpressing the  
single transcription factor HAT4 (8). Flu-  
rescent probes representing mRNA from  
wild-type and HAT4-transgenic plants were  
labeled with fluorescein and lissamine, re-  
spectively; the two probes were then mixed  
and hybridized to a single array. An intense  
hybridization signal was observed at the  
position of the HAT4 cDNA in the liss-  
amine-specific scan (Fig. 1D), but not in the  
fluorescein-specific scan of the same array  
(Fig. 1C). Calibration with AChR mRNA  
added to the fluorescein and lissamine  
cDNA synthesis reactions at dilutions of  
1:10,000 (Fig. 1C) and 1:100 (Fig. 1D),  
respectively, revealed a 50-fold elevation of  
HAT4 mRNA in the transgenic line rela-  
tive to its abundance in wild-type plants  
(Table 2). This magnitude of HAT4 over-  
expression matched that inferred from the  
Northern (RNA) analysis within a factor of  
2 (Fig. 2 and Table 2). Expression of all the  
other genes monitored on the array differed  
by less than a factor of 5 between HAT4-  
transgenic and wild-type plants (Fig 1, C



Gene expression monitored with the use of cDNA microarrays. Fluorescent scans represented in  
locolor correspond to hybridization intensities. Color bars were calibrated from the signal obtained  
ie use of known concentrations of human AChR mRNA in independent experiments. Numbers and  
on the axes mark the position of each cDNA. (A) High-sensitivity fluor escein scan after hybridization  
u rescein-labeled cDNA derived from wild-type plants. (B) Same array as in (A) but scanned at  
ate sensitivity. (C and D) A single array was probed with a 1:1 mixture of fluorescein-labeled cDNA  
wild-type plants and lissamine-labeled cDNA from HAT4-transgenic plants. The single array was  
anned successively to detect the fluorescein fluorescence corresponding t mRNA from wild-type  
(C) and the lissamine fluorescence corresponding to mRNA from HAT4-transgenic plants (D). (E  
A single array was probed with a 1:1 mixture of fluorescein-labeled cDNA from root tissue and  
ne-labeled cDNA from leaf tissue. The single array was then scanned successively to detect the  
cein fluorescence corresponding to mRNAs expressed in roots (E) and the lissamine fluorescence  
ponding to mRNAs expressed in leaves (F).

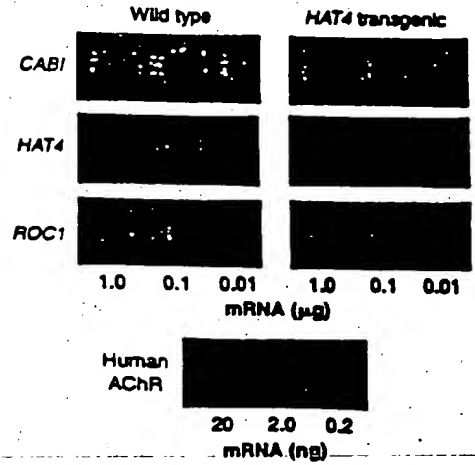


Fig. 2. Gene expression monitored with RNA  
(Northern) blot analysis. Designated amounts of  
mRNA from wild-type and HAT4-transgenic  
plants were spotted onto nylon membranes and  
probed with the cDNAs indicated. Purified human  
AChR mRNA was used for calibration.

and D, and Table 2). Hybridization of fluorescein-labeled glucocorticoid receptor cDNA (Fig. 1C) and lissamine-labeled TRP4 cDNA (Fig. 1D) verified the presence of the negative control targets and the lack of optical cross talk between the two fluorophores.

To explore a more complex alteration in expression patterns, we performed a second two-color hybridization experiment with fluorescein- and lissamine-labeled probes prepared from root and leaf mRNA, respectively. The scanning sensitivities for the two fluorophores were normalized by matching the signals resulting from AChR

mRNA, which was added to both cDNA synthesis reactions at a dilution of 1:1000 (Fig. 1, E and F). A comparison of the scans revealed widespread differences in gene expression between root and leaf tissue (Fig. 1, E and F). The mRNA from the light-regulated *CAB1* gene was ~500-fold more abundant in leaf (Fig. 1F) than in root tissue (Fig. 1E). The expression of 26 other genes differed between root and leaf tissue by more than a factor of 5 (Fig. 1, E and F).

The *HAT4*-transgenic line we examined has elongated hypocotyls, early flowering, poor germination, and altered pigmentation (8). Although changes in expression were

observed for *HAT4*, large changes in expression were not observed for any of the other 44 genes we examined. This was somewhat surprising, particularly because comparative analysis of leaf and root tissue identified 27 differentially expressed genes. Analysis of an expanded set of genes may be required to identify genes whose expression changes upon *HAT4* overexpression; alternatively, a comparison of mRNA populations from specific tissues of wild-type and *HAT4*-transgenic plants may allow identification of downstream genes.

At the current density of robotic printing, it is feasible to scale up the fabrication process to produce arrays containing 20,000 cDNA targets. At this density, a single array would be sufficient to provide gene-specific targets encompassing nearly the entire repertoire of expressed genes in the *Arabidopsis* genome (2). The availability of 20,274 ESTs from *Arabidopsis* (1, 9) would provide a rich source of templates for such studies.

The estimated 100,000 genes in the human genome (10) exceeds the number of *Arabidopsis* genes by a factor of 5 (2). This modest increase in complexity suggests that similar cDNA microarrays, prepared from the rapidly growing repertoire of human ESTs (1), could be used to determine the expression patterns of tens of thousands of human genes in diverse cell types. Coupling an amplification strategy to the reverse transcription reaction (11) could make it feasible to monitor expression even in minute tissue samples. A wide variety of acute and chronic physiological and pathological conditions might lead to characteristic changes in the patterns of gene expression in peripheral blood cells or other easily sampled tissues. In concert with cDNA microarrays for monitoring complex expression patterns, these tissues might therefore serve as sensitive *in vivo* sensors for clinical diagnosis. Microarrays of cDNAs could thus provide a useful link between human gene sequences and clinical medicine.

**Table 2.** Gene expression monitoring by microarray and RNA blot analyses; tg, *HAT4*-transgenic. See Table 1 for additional gene information. Expression levels (w/w) were calibrated with the use of known amounts of human AChR mRNA. Values for the microarray were determined from microarray scans (Fig. 1); values for the RNA blot were determined from RNA blots (Fig. 2).

Gene	Expression level (w/w)	
	Microarray	RNA blot
<i>CAB1</i>	1:48	1:83
<i>CAB1</i> (tg)	1:120	1:150
<i>HAT4</i>	1:8300	1:8300
<i>HAT4</i> (tg)	1:150	1:210
<i>ROC1</i>	1:1200	1:1800
<i>ROC1</i> (tg)	1:260	1:1300

**Table 1.** Sequences contained on the cDNA microarray. Shown is the position, the known or putative function, and the accession number of each cDNA in the microarray (Fig. 1). All but three of the ESTs used in this study matched a sequence in the database. NADH, reduced form of nicotinamide adenine dinucleotide; ATPase, adenosine triphosphatase; GTP, guanosine triphosphate.

Position	cDNA	Function	Accession number
a1, 2	AChR	Human AChR	-
a3, 4	EST3	Actin	H36236
a5, 6	EST6	NADH dehydrogenase	Z27010
a7, 8	AAC1	Actin 1	M20016
a9, 10	EST12	Unknown	U365941
a11, 12	EST13	Actin	T45783
b1, 2	<i>CAB1</i>	Chlorophyll a/b binding	M85150
b3, 4	EST17	Phosphoglycerate kinase	T44490
b5, 6	GA4	Gibberellic acid biosynthesis	L37126
b7, 8	EST19	Unknown	U365951
b9, 10	<i>GBF-1</i>	G-box binding factor 1	X63894
b11, 12	EST23	Elongation factor	X52256
c1, 2	EST29	Aldolase	T04477
c3, 4	<i>GBF-2</i>	G-box binding factor 2	X63895
c5, 6	EST34	Chloroplast protease	R87034
c7, 8	EST35	Unknown	T14152
c9, 10	EST41	Catalase	T22720
c11, 12	rGR	Rat glucocorticoid receptor	M14053
d1, 2	EST42	Unknown	U365961
d3, 4	EST45	ATPase	J04185
d5, 6	<i>HAT1</i>	Homeobox-leucine zipper 1	U09332
d7, 8	EST46	Light harvesting complex	T04063
d9, 10	EST49	Unknown	T76267
d11, 12	<i>HAT2</i>	Homeobox-leucine zipper 2	U09335
e1, 2	<i>HAT4</i>	Homeobox-leucine zipper 4	M90394
e3, 4	EST50	Phosphoribulokinase	T04344
e5, 6	<i>HAT5</i>	Homeobox-leucine zipper 5	M90416
e7, 8	EST51	Unknown	Z33675
e9, 10	<i>HAT22</i>	Homeobox-leucine zipper 22	U09336
e11, 12	EST52	Oxygen evolving	T21749
f1, 2	EST59	Unknown	Z34607
f3, 4	<i>KNAT1</i>	Knotted-like homeobox 1	U14174
f5, 6	EST60	RuBisCO small subunit	X14564
f7, 8	EST69	Translation elongation factor	T42799
f9, 10	<i>PPH1</i>	Protein phosphatase 1	U34803
f11, 12	EST70	Unknown	T44621
g1, 2	EST75	Chloroplast protease	T43698
g3, 4	EST78	Unknown	R65481
g5, 6	<i>ROC1</i>	Cyclophilin	L14844
g7, 8	EST82	GTP binding	X59152
g9, 10	EST83	Unknown	Z33795
g11, 12	EST84	Unknown	T45278
h1, 2	EST91	Unknown	T13832
h3, 4	EST96	Unknown	R64816
h5, 6	<i>SAR1</i>	Synaptobrevin	M90418
h7, 8	EST100	Light harvesting complex	Z18205
h9, 10	EST103	Light harvesting complex	X03909
h11, 12	<i>TRP4</i>	Yeast tryptophan biosynthesis	X04273

proprietary sequence of Stratagene (La Jolla, California).

†No match in the database; novel EST.



nt EST database (dbEST release 091495) National Center for Biotechnology Information, Bethesda, MD) contains a total of 322,225 including 255,645 from the human genome and 64 from Arabidopsis. Access is available via Wide Web (<http://www.ncbi.nlm.nih.gov>).

erowitz and R. E. Pruitt, *Science* 229, 1214 (1986); E. Pruitt and E. M. Meyerowitz, *J. Mol. Biol.* (1986); I. Hwang et al., *Plant J.* 1, 367 (1991); et al., *Plant Mol. Biol.* 24, 685 (1994); L. Leu, *Mol. Gen. Genet.* 245, 390 (1994).

thesis, Stanford University (1995); Brown, in preparation. Microarrays were on poly-L-lysine-coated microscope (gma) with a custom-built arraying machine one printing tip. The tip loaded 1 µl of PCR (0.5 mg/ml) from 96-well microtiter plates (sited -0.005 µl per slide on 40 slides at a of 500 µm. The printed slides were rehydrat- hours in a humid chamber, snap-dried at r 1 min, rinsed in 0.1% SDS, and treated i% succinic anhydride prepared in buffer j of 50% 1-methyl-2-pyrrolidinone and c acid. The cDNA on the slides was dena- distilled water for 2 min at 90°C immediately ie. Microarrays were scanned with a laser nt scanner that contained a computer-con- stage and a microscope objective. A mixed line laser allowed sequential excitation of orophores. Emitted light was split accord- vavelength and detected with two photomul- is. Signals were read into a PC with the use t analog-to-digital board. Additional details ray fabrication and use may be obtained by e-mail ([pbrown@crgm.stanford.edu](mailto:pbrown@crgm.stanford.edu)).

ubel et al., Eds., *Current Protocols in Mology* (Greene & Wiley Interscience, New 4), pp. 4.3.1-4.3.4.

yated [poly(A)<sup>+</sup>] mRNA was prepared from with the use of Oligotex-dT resin (Qiagen). ranscription (RT) reactions were carried out itaScript RT-PCR kit (Stratagene) modified it: 50-µl reactions contained 0.1 µg/µl of is mRNA, 0.1 ng/µl of human AChR .05 µg/µl of oligo(dT) (21-mer), 1× first fter, 0.03 U/µl of ribonuclease block, 500 adenine triphosphate (dATP), 500 µM nosine triphosphate, 500 µM dTTP, 40 cytosine triphosphate (dCTP), 40 µM flu- 12-dCTP (or isamine-5-dCTP), and 0.03 ataScript reverse transcriptase. Reactions bated for 60 min at 37°C, precipitated with nd resuspended in 10 µl of TE (10 mM trs- 1 mM EDTA, pH 8.0). Samples were then 3 min at 94°C and chilled on ice. The RNA aded by adding 0.25 µl of 10 N NaOH y a 10-min incubation at 37°C. The sam- neutralized by addition of 2.5 µl of 1 M 8.0) and 0.25 µl of 10 N HCl and precip- ethanol. Pellets were washed with 70% ined to completion in a speedvac, resus- 10 µl of H<sub>2</sub>O, and reduced to 3.0 µl in a . Fluorescent nucleotide analogs were ob- n New England Nuclear (DuPont).

on reactions contained 1.0 µl of fluorescent hesis product (5) and 1.0 µl of hybridization x saline sodium citrate (SSC) and 0.2% 2.0-µl probe mixtures were aliquoted onto uray surface and covered with cover slips und). Arrays were transferred to a hybrid- mber (3) and incubated for 18 hours at ys were washed for 5 min at room temper- ) in low-stringency wash buffer (1× SSC SDS), then for 10 min at room temperature gency wash buffer (0.1× SSC and 0.1% ys were scanned in 0.1× SSC with the use ence laser-scanning device (3).

t poly(A)<sup>+</sup> mRNA (4, 5) were spotted onto rbanes (Nytran) and crosslinked with ul- hit with the use of a Stratalinker 1800 e). Probes were prepared by random h the use of a Prime-It II kit (Stratagene) in ce of [<sup>32</sup>P]dATP. Hybridizations were car- cording to the instructions of the manu-

tacturer. Quantitation was performed on a Phos- phorimager (Molecular Dynamics).

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12. The laser fluorescent scanner was designed and fabri- cated in collaboration with S. Smith of Stanford Univer- sity. Scanner and analysis software was developed by R. X. Xia. The succinic anhydride reaction was sugges- ted by J. Mulligan and J. Van Ness of Darwin Molecular Corporation. Thanks to S. Theologis, C. Somerville, K. Yamamoto, and members of the laboratories of R.W.C. and P.O.B. for critical comments. Supported by the Howard Hughes Medical Institute and by grants from NIH (R21HG00450) (P.O.B.) and R37AG00196 (R.W.D.) and from NSF (MCB9106011) (R.W.D.) and by an NSF graduate fellowship (D.S.). P.O.B. is an assistant investigator of the Howard Hughes Medical Institute.

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# Gene Therapy in Peripheral Blood Lymphocytes and Bone Marrow for ADA<sup>-</sup> Immunodeficient Patients

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Adenosine deaminase (ADA) deficiency results in severe combined immunodeficiency, the first genetic disorder treated by gene therapy. Two different retroviral vectors were used to transfer ex vivo the human ADA minigene into bone marrow cells and peripheral blood lymphocytes from two patients undergoing exogenous enzyme replacement therapy. After 2 years of treatment, long-term survival of T and B lymphocytes, marrow cells, and granulocytes expressing the transferred ADA gene was demonstrated and resulted in normalization of the immune repertoire and restoration of cellular and humoral immunity. After discontinuation of treatment, T lymphocytes, derived from transduced peripheral blood lymphocytes, were progressively replaced by marrow-derived T cells in both patients. These results indicate successful gene transfer into long-lasting progenitor cells, producing a functional multilineage progeny.

Severe combined immunodeficiency associated with inherited deficiency of ADA (1) is usually fatal unless affected children are kept in protective isolation or the immune system is reconstituted by bone marrow transplantation from a human leukocyte antigen (HLA)-identical sibling donor (2). This is the therapy of choice, although it is available only for a minority of patients. In recent years, other forms of therapy have been developed, including transplants from haploidentical donors (3, 4), exogenous enzyme replacement (5), and somatic-cell gene therapy (6-9).

We previously reported a preclinical model in which ADA gene transfer and expression

successfully restored immune functions in human ADA-deficient (ADA<sup>-</sup>) peripheral blood lymphocytes (PBLs) in immunodeficient mice in vivo (10, 11). On the basis of these preclinical results, the clinical application of gene therapy for the treatment of ADA<sup>-</sup> SCID (severe combined immunodeficiency disease) patients who previously failed exogenous enzyme replacement therapy was approved by our Institutional Ethical Committees and by the Italian National Committee for Bioethics (12). In addition to evaluating the safety and efficacy of the gene therapy procedure, the aim of the study was to define the relative role of PBLs and hematopoietic stem cells in the long-term reconstitution of immune functions after retroviral vector-mediated ADA gene transfer. For this purpose, two structurally identical vectors expressing the human ADA complementary DNA (cDNA), distinguishable by the presence of alternative restriction sites in a nonfunctional region of the viral long-terminal repeat (LTR), were used to transduce PBLs and bone marrow (BM) cells independently. This procedure allowed identification of the origin of

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